

Q.Nguyen

Page 1 of 7

H10

12-22-00

1632 P2

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/462,517

DATE: 11/21/2000  
TIME: 11:52:46

Input Set : A:\sequence  
Output Set: N:\CRF3\11212000\I462517.raw

3 <110> APPLICANT: Aurora Biosciences Corporation  
4 Zucker, Charles  
5 Mendlein, John  
6 Sun, Yumei  
7 Tsunoda, Susan  
8 Sierralta, Jimena  
10 <120> TITLE OF INVENTION: Compositions And Methods For Identifying Modulators and Transducisomes  
12 <130> FILE REFERENCE: AURO1210-1  
14 <140> CURRENT APPLICATION NUMBER: 09/462,517  
15 <141> CURRENT FILING DATE: 2000-05-18  
17 <160> NUMBER OF SEQ ID NOS: 16  
19 <170> SOFTWARE: PatentIn version 3.0  
21 <210> SEQ ID NO: 1  
22 <211> LENGTH: 674  
23 <212> TYPE: PRT  
24 <213> ORGANISM: Drosophila melanogaster  
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31 Met Val Thr Leu Asp Lys Thr Gly Lys Ser Phe Gly Ile Cys Ile  
32 20 25 30  
34 Val Arg Gly Glu Val Lys Asp Ser Pro Asn Thr Lys Thr Gly Ile  
35 35 40 45  
37 Phe Ile Lys Gly Ile Val Pro Asp Ser Pro Ala His Leu Cys Gly Arg  
38 50 55 60  
40 Leu Lys Val Gly Asp Arg Ile Leu Ser Leu Asn Gly Lys Asp Val Arg  
41 65 70 75 80  
43 Asn Ser Thr Glu Gln Ala Val Ile Asp Leu Ile Lys Glu Ala Asp Phe  
44 85 90 95  
46 Lys Ile Glu Leu Glu Ile Gln Thr Phe Asp Lys Ser Asp Glu Gln Gln  
47 100 105 110  
49 Ala Lys Ser Asp Pro Arg Ser Asn Gly Tyr Met Gln Ala Lys Asn Lys  
50 115 120 125  
52 Phe Asn Gln Glu Gln Thr Thr Asn Asn Ala Ser Gly Gly Gln Gly  
53 130 135 140  
55 Met Gly Gln Gly Gln Gly Gln Gly Met Ala Gly Met Asn Arg  
56 145 150 155 160  
58 Gln Gln Ser Met Gln Lys Arg Asn Thr Thr Phe Thr Ala Ser Met Arg  
59 165 170 175  
61 Gln Lys His Ser Asn Tyr Ala Asp Glu Asp Asp Glu Asp Thr Arg Asp  
62 180 185 190  
64 Met Thr Gly Arg Ile Arg Thr Glu Ala Gly Tyr Glu Ile Asp Arg Ala  
65 195 200 205  
67 Ser Ala Gly Asn Cys Lys Leu Asn Lys Gln Glu Lys Asp Arg Asp Lys  
68 210 215 220  
70 Glu Gln Glu Asp Glu Phe Gly Tyr Thr Met Ala Lys Ile Asn Lys Arg  
71 225 230 235 240

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Input Set : A:\sequence  
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73 Tyr Asn Met Met Lys Asp Leu Arg Arg Ile Glu Val Gln Arg Asp Ala  
 74 245 250 255  
 76 Ser Lys Pro Leu Gly Leu Ala Leu Ala Gly His Lys Asp Arg Gln Lys  
 77 260 265 270  
 79 Met Ala Cys Phe Val Ala Gly Val Asp Pro Asn Gly Ala Leu Gly Ser  
 80 275 280 285  
 82 Val Asp Ile Lys Pro Gly Asp Glu Ile Val Glu Val Asn Gly Asn Val  
 83 290 295 300  
 85 Leu Lys Asn Arg Cys His Leu Asn Ala Ser Ala Val Phe Lys Asn Val  
 86 305 310 315 320  
 88 Asp Gly Asp Lys Leu Val Met Ile Thr Ser Arg Arg Lys Pro Asn Asp  
 89 325 330 335  
 91 Glu Gly Met Cys Val Lys Pro Ile Lys Lys Phe Pro Thr Ala Ser Asp  
 92 340 345 350  
 94 Glu Thr Lys Phe Ile Phe Asp Gln Phe Pro Lys Ala Arg Thr Val Gln  
 95 355 360 365  
 97 Val Arg Lys Glu Gly Phe Leu Gly Ile Met Val Ile Tyr Gly Lys His  
 98 370 375 380  
 100 Ala Glu Val Gly Ser Gly Ile Phe Ile Ser Asp Leu Arg Glu Gly Ser  
 101 385 390 395 400  
 103 Asn Ala Glu Leu Ala Gly Val Lys Val Gly Asp Met Leu Leu Ala Val  
 104 405 410 415  
 106 Asn Gln Asp Val Thr Leu Glu Ser Asn Tyr Asp Asp Ala Thr Gly Leu  
 107 420 425 430  
 109 Leu Lys Arg Ala Glu Gly Val Val Thr Met Ile Leu Leu Thr Leu Lys  
 110 435 440 445  
 112 Ser Glu Glu Ala Ile Lys Ala Glu Lys Ala Ala Glu Glu Lys Lys  
 113 450 455 460  
 115 Glu Glu Ala Lys Lys Glu Glu Lys Pro Gln Glu Pro Ala Thr Ala  
 116 465 470 475 480  
 118 Glu Ile Lys Pro Asn Lys Lys Ile Leu Ile Glu Leu Lys Val Glu Lys  
 119 485 490 495  
 121 Lys Pro Met Gly Cys His Arg Leu Arg Arg Gln Lys Gln Pro Cys His  
 122 500 505 510  
 124 Asp Trp Leu Cys Asn His Pro Arg Leu Ser Gly Gly Gln Val Ala Ala  
 125 515 520 525  
 127 Asp Lys Arg Leu Lys Ile Phe Asp His Ile Cys Asp Ile Asn Gly Thr  
 128 530 535 540  
 130 Pro Ile His Val Gly Ser Met Thr Thr Leu Lys Val His Gln Leu Phe  
 131 545 550 555 560  
 133 His Thr Thr Tyr Glu Lys Ala Val Thr Leu Thr Val Phe Arg Ala Asp  
 134 565 570 575  
 136 Pro Pro Glu Leu Glu Lys Phe Asn Val Asp Leu Met Lys Lys Ala Gly  
 137 580 585 590  
 139 Lys Glu Leu Gly Leu Ser Leu Ser Pro Asn Glu Ile Gly Cys Thr Ile  
 140 595 600 605  
 142 Ala Asp Leu Ile Gln Gly Gln Tyr Pro Glu Ile Asp Ser Lys Leu Gln  
 143 610 615 620  
 145 Arg Gly Asp Ile Ile Thr Lys Phe Asn Gly Asp Ala Leu Glu Gly Leu

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146 625          630          635          640
148 Pro Phe Gln Val Cys Tyr Ala Leu Phe Lys Gly Ala Asn Gly Lys Val
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151 Ser Met Glu Val Thr Arg Pro Lys Pro Thr Leu Arg Thr Glu Ala Pro
152           660          665          670
154 Lys Ala
157 <210> SEQ ID NO: 2
158 <211> LENGTH: 2059
159 <212> TYPE: DNA
160 <213> ORGANISM: Drosophila melanogaster
162 <400> SEQUENCE: 2
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165 qacaagacgg gcaagaagtc ctteggatc tgcataatgc gcggcgagggt gaaaggatttcg    120
167 cccaaaccca agacaacccgg cattttcata aaggggatgg tgcccgacag tccccgcgtat   180
169 ctgtgtggtc gcctaaagggt tggcgtatcg atcccttcgc tcaacggaaa ggatgtgcgc  240
171 aactccacccg aacaggcggt catcgatctc atcaaggagg cgacttcaa gatcgagctg  300
173 gagattcaaga ctttcgacaa gagcgtatgg caaggccacc agtcgatggc gcggaaqcaat 360
175 ggctacatgc aggccaagaa caagttcaat cggaggcaga ccaccaacaa caatgcgttcc 420
177 ggagggtcagg gaatggggca aagtcagggt cagggtcagg gaatggctgg catgaacccgg 480
179 caaataccta tgcagaacgc gaataccaca ttcaacggctt cgtatgcgttca gaaqcatagt 540
181 aactaccccg acgaggatga cgaggacacc cgaggacatga cgggttcgtat tcgcacggag 600
183 ggggttatg agatcgatcg agcctccqcc ggttaatttgc aacttaataa gcaggaaaag 660
185 gatcgacaca aggaggcaga agatgaattt ggtacacacgc tggctaaatg caacaaggcg 720
187 tacaacatgc tggatgttgc tgcgtggatc gagggtcagg gggacgcccgg caagccactg 780
189 qqactccgcac tgcgtggca caaqgaccgc cagaagatgg cttgttttg tggcgtgtg 840
191 gatecccaacg gggcattggg cagcgtggac attaagccgg ggcacgagat cgtcgagggtc 900
193 aacggcaatg tgcctaaagaa tgcgtgccac ttgaacgcctt cggccgtgtt caagagcggt 960
195 gatggggata agctcgatg gatcacccatcg cgaacgcaacgc ccaacatgtt gggcatgtgc 1020
197 gtcaagccca tcaaaaagggtt ccccaccccg tctgtatgaa ctaaggtttat cticgaccag 1080
199 ttcccaagg cgcgcacccgtt gcaagggtcggc aaggagggtt cttggccatc atggtcatct 1140
201 atggcaagca cgcgtggatg ggcagtggca tttttcatttc ggtatctgaga gagggtatcg 1200
203 atggcgagtt ggcggcggtg aaagtggcg acatgtgtgtt ggcgtttaat caggatgtaa 1260
205 cactggatc caactacatg gatcgactcg gactgtgtt acgtggccgg ggcgttagtgc 1320
207 ccatgtatctt attgacttc aagagcgagg aggcataaa ggtgtggatgg gcaagcggaaag 1380
209 aaaaaaagaa ggaggaggcc aagaaagagg agggaaaagcc acaggaaaccc gccacacccg 1440
211 agatcaagcc gaacaaaaaaat atactcatttgc agtttggatggt gggaaaagaaag ccaatggcg 1500
213 tcacgttgc cggcgccaa gacaaccatg tcacgactgg ctgtgtatc acccacgtt 1560
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221 aaaagttaa cgttgacccat ataaaaaaag caggcaagggc gtcggccgtg tcgtgttcc 1800
223 ccaacgaaat tggatgcacc atcgccgact tggatcaagg acaataccgg gagattgaca 1860
225 gcaactcgca gcggcgccat attatccaca attcaatggc gatgccttgg agggtcttcc 1920
227 gttcccgatgt tgcgtacgtt tggatcaagg aaccaacggc aagggtatcga tggaaagtgtac 1980
229 acgacccaaag cccactctac gtacggaggc acccaacggcc tagagacgtt cctcatttc 2040
231 ctctccgtat cgaaggatgt 2059
234 <210> SEQ ID NO: 3
235 <211> LENGTH: 93
236 <212> TYPE: PRT

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Input Set : A:\sequence  
Output Set: N:\CRF3\11212000\I462517.raw

237 <213> ORGANISM: artificial  
239 <220> FEATURE:  
240 <223> OTHER INFORMATION: PSD-1  
242 <400> SEQUENCE: 3  
244 Met Glu Tyr Glu Glu Ile Thr Leu Glu Arg Gly Asn Ser Gly Leu Gly  
245 1 5 10 15  
247 Phe Ser Ile Ala Gly Gly Thr Asp Asn Pro His Ile Gly Asp Asp Pro  
248 20 25 30  
250 Ser Ile Phe Ile Thr Lys Ile Ile Pro Gly Gly Ala Ala Ala Gln Asp  
251 35 40 45  
253 Gly Arg Leu Arg Val Asn Asp Ser Ile Leu Phe Val Asn Glu Val Asp  
254 50 55 60  
256 Val Arg Glu Val Thr His Ser Ala Ala Val Glu Ala Leu Lys Glu Ala  
257 65 70 75 80  
259 Gly Ser Ile Val Arg Leu Tyr Val Met Arg Arg Lys Pro  
260 85 90  
262 <210> SEQ ID NO: 4  
263 <211> LENGTH: 93  
264 <212> TYPE: PRT  
265 <213> ORGANISM: Artificial  
267 <220> FEATURE:  
268 <223> OTHER INFORMATION: PSD95-2  
270 <400> SEQUENCE: 4  
272 Glu Lys Val Met Glu Ile Lys Leu Ile Lys Gly Pro Lys Gly Leu Gly  
273 1 5 10 15  
275 Phe Ser Ile Ala Gly Gly Val Gly Asn Gln His Ile Pro Gly Asp Asn  
276 20 25 30  
278 Ser Ile Tyr Val Thr Lys Ile Ile Glu Gly Gly Ala Ala His Lys Asp  
279 35 40 45  
281 Gly Arg Leu Gln Ile Gly Asp Lys Ile Leu Ala Val Asn Ser Val Gly  
282 50 55 60  
284 Leu Glu Asp Val Met His Glu Asp Ala Val Ala Ala Leu Lys Asn Thr  
285 65 70 75 80  
287 Tyr Asp Val Val Tyr Leu Lys Val Ala Lys Pro Ser Asn  
288 85 90  
290 <210> SEQ ID NO: 5  
291 <211> LENGTH: 87  
292 <212> TYPE: PRT  
293 <213> ORGANISM: artificial  
295 <220> FEATURE:  
296 <223> OTHER INFORMATION: PSD95-3  
298 <400> SEQUENCE: 5  
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301 1 5 10 15  
303 Phe Asn Ile Val Gly Gly Glu Asp Gly Glu Gly Ile Phe Ile Ser Phe  
304 20 25 30  
306 Ile Leu Ala Gly Gly Pro Ala Asp Leu Ser Gly Glu Leu Arg Lys Gly  
307 35 40 45  
309 Asp Gln Ile Leu Ser Val Asn Gly Val Asp Leu Arg Asn Ala Ser His

RAW SEQUENCE LISTING DATE: 11/21/2000  
 PATENT APPLICATION: US/09/462,517 TIME: 11:52:46

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 Output Set: N:\CRF3\11212000\I462517.raw

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310      50          55          60
312 Glu Gln Ala Ala Ile Ala Leu Lys Asn Ala Gly Gln Thr Val Thr Ile
313 65          70          75          80
315 Ile Ala Gln Tyr Lys Pro Glu
316          85
318 <210> SEQ ID NO: 6
319 <211> LENGTH: 87
320 <212> TYPE: PRT
321 <213> ORGANISM: artificial
323 <220> FEATURE:
324 <223> OTHER INFORMATION: dlg-3
326 <400> SEQUENCE: 6
328 Arg Glu Pro Arg Thr Ile Thr Ile Gln Lys Gly Pro Gln Gly Leu Gly
329 1          5          10          15
331 Phe Asn Ile Val Gly Gly Glu Asp Gly Gln Gly Ile Tyr Val Ser Phe
332          20          25          30
334 Ile Leu Ala Gly Gly Pro Ala Asp Leu Gly Ser Glu Leu Lys Arg Gly
335          35          40          45
337 Asp Gln Leu Leu Ser Val Asn Asn Val Asn Leu Thr His Ala Thr His
338          50          55          60
340 Glu Glu Ala Ala Gln Ala Leu Lys Thr Ser Gly Gly Val Val Thr Leu
341 65          70          75          80
343 Leu Ala Gln Tyr Arg Pro Glu
344          85
346 <210> SEQ ID NO: 7
347 <211> LENGTH: 88
348 <212> TYPE: PRT
349 <213> ORGANISM: artificial
351 <220> FEATURE:
352 <223> OTHER INFORMATION: nnos
354 <400> SEQUENCE: 7
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357 1          5          10          15
359 Gly Phe Leu Val Lys Glu Arg Val Ser Lys Pro Pro Val Ile Ile Ser
360          20          25          30
362 Asp Leu Ile Arg Gly Gly Ala Ala Glu Gln Ser Gly Leu Ile Gln Ala
363          35          40          45
365 Gly Asp Ile Ile Leu Ala Val Asn Asp Arg Pro Leu Val Asp Leu Ser
366          50          55          60
368 Tyr Asp Ser Ala Leu Glu Val Leu Arg Gly Ile Ala Ser Glu Thr His
369 65          70          75          80
371 Val Val Leu Ile Leu Arg Gly Pro
372          85
374 <210> SEQ ID NO: 8
375 <211> LENGTH: 88
376 <212> TYPE: PRT
377 <213> ORGANISM: artificial
379 <220> FEATURE:
380 <223> OTHER INFORMATION: inaD-3

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FYI:

**Please Note:**

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY  
PATENT APPLICATION: US/09/462,517

DATE: 11/21/2000  
TIME: 11:52:47

Input Set : A:\sequence  
Output Set: N:\CRF3\11212000\I462517.raw

L:568 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16

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